

Figure 1

ggegecegee egeogeooge eeggeeceg getgeeteee tteeteete ectetetite teeetigege tegetegete getegeecte ggegeatggg coergegeeg ggereegggg cetegggeeg cetggeetee ggggteeet aggereggge gtgggegggg cagereggee tgaegeagee tetgtaceee 200 accaccacca ccaccagggc cggcggcggc ggctgccccg agggacgggg ccctaggcgg tggcgATGGG GGCCGTCCGG ATCGCGCCCG GCCTGGCGCT M G A U R I A P G L A L GCTGCTCTGC TGCCCGGTGC TCAGCTCCGC GTACGCGCTG GTGGATGCAG ATGACGTCAT GACCAAAGAG GAGCAGATCT TCCTGCTGCA CCGCGCCCAG 400 LLC CPULS SANYAL VORD DUNTKE EQIFLLH RAQ GCCCRGTGCC AGRAGGGGCT CARAGARGTC CTGCRGAGGC CAGCTGRCAT RATGGRATCA GACARAGGAT GGGCTTCTGC ATCCACATCA GGGAAGCCTA 500 A Q C Q K R L K E U L Q R P A D I M E S D K G U A S A S T S G K P K AGAAAGAGAA GGCATCTGGG AAGCTCTACC CTGAGTCCGA GGAGGACAAG GAGGTGCCCA CTGGCAGCAG GCACCGAGGG CGCCCTGCC TGCCCGAGTG KEK ASG KLYPESE EDKEUPT GSR HRG RPCL PE W GGACCACATC CITIGGTGGC CGCTGGGGGC ACCAGGTGAG GTGGTGGCTG TGCCCTGTCC CGACTACATT TATGACTTCA ATCACAAAGG CCATGCCTAC DHILCUPLGAPGE UUAU PCP DYIYD FN HKG CGTCGCTGTG ACCGCARTGG CAGCTGGGAG CTGGTGCCTG GACACCAG GACGTGGGCC AACTACAGCG AGTGTGTCAA GTTCCTGACC AACGAGACTC RRCD RNG SWELUPG HNR TWA_NYSE CUKFLT NETA GTGAACGGGA GGTGTTTGAC CGC<u>CTGGGCA TGATCTACAC CGTGGGCTAC TCCGTGTCGC TGGCCTCCCT CACCGTGGCC GTGCTCATCC TGGCC</u>TACTT 900 ERE U F D R L G M I Y T U G Y S U S L A S L U A U L I L A Y F CAGGCGGCTG CACTGCACAC GEAACTACAT CCACATGCAC CIGTICCTGI CCTICATGCI ICGCGCCGIG AGCAICTICG ICAAGGACGC GGIGCTCIAC RRL H C T R N Y I H M H L F L S F M L R A U S I F U K D A U L Y TEGGGGGGG CGCTCGACGA GGCCGACGC CTCACGGAGG AAGAGCTGCG CGCCATCGCCCCC CGCCGCCCAC CGCCGCCCCC GGCTACGCGG S G A T L D E A E R L T E E E L R A I A Q A P P P P T A R A G Y A G III GCTGCAGGGT AGCTGTGACC TICTTCCTTT ATTTCCTGGC CACCARCTAC TACTGGATTC TGGTGGAGGG GCTGTACCTG CATAGTCTCA TCTTCATGGC CRUAUT FFLY FLATNY Y M I L U E G L Y L H S L I F M A ${f IV}$ CTICITOTOR GRGARGARGT ACCTOTOGGG CTICACGGTC TICGGCTGGG GTCTGCCGC CGTCTTCGTG GCTGTGTGGG TCRGCGTGAG AGCCACCTG FFS EKKY L M G FTU F G M G L P A U F U A U M U S U R A T L GCCARCACO GGTGCTGGGA CTIGAGCTCC GGGAACARGA AGTGGATCAT CCAGGTGCCC ATCCTGGCCT CTATIGTGCT CARCTICATC TIGTICATCA 1400 ANT G CHOLSS GNKK HII QUPILAS IUL NFI LFIN ACATCGTCCG GGTGCTCCC ACDAAGCTGC GGGAGACCAA TGCCGGCCGG TGTGACACGC GGCAGCAGTA CCGGAAGCTG CTCAAATCCA CACTGGTGCT I URULATKLAETN AGRCDTR QQY RKLLKSTLUL ${f V}{f I}$ CATGCCGCTC TITGGCGTCC ACTACATCGT CTTCATGGCC ACGCCGTACA CCGAGGTCTC AGGGACGCTC TGGCAAGTCC AGATGCACTA CGAGATGCTD MPLF6UHY VII <u>Y</u> IU F M A T P Y T E U S G T L H Q U Q M H Y E M L TICARCICCT TCCAGGGATT ITITGICGCC ATCATATACT GITTCIGCAA TGGCCGGGGTA CAGGCCGGGA TCAAGAAAATC CIGGAGCCGC IGGACACTGG QGFFUAIIYCFCNGEUQAEIKKS USB UTLA CCCTGGRCTT CARGCGCARG GCCCGARGTG GGAGCAGCAG TTACAGCTAC GGCCCGATGG TGTCTCACAC GAGCGTGACC AACGTAGGCC CCCGGCGGG 1800 L D F K A K A A S G S S S Y S Y G P M U S H T S U T N U G P R A G ACTIGGECTG CECCTCAGCC CCCGCCTGCT GCCGCCGCT GCCGCCACCA CCACCCACC CACCAACGGC CACCCCCGA TCCCGGGCCA CACCAAGCCA LGL PLSP R LL PAA AATT TAT T N G H PP I P G H T K P GGGGCCCGGA CCCTCCCGGC CACACCACCT GCCACGGCTG CTCCCAAGGA CGATGGGTTC CTCAACGGCT CCTGCTCGGG GCTGGACGAG GAGGCCTCCG 2000 GAPT L PATPPATAA PKD DGF L NGS CSG L DE EASA CGCCGGAGCG GCCTCCCGCC CTGCTGCAGG AGGAGTGGGA GACGGTCATG TGAtcgggga cctgtgccag ggttggactc gtggacataa gggccgacag PERPPALLQEEHETUM. 2177 acquectana agacagaaga tiqqaaqti qeccaataag agatagagat gagaagaana aacaanaana aacaanaa

SEQ. ID No. 1

- and like a like the all considers all social and considerable belong the best by the be

	Figure 2	
dPTH1	ATGGGGGCCG INCCGGATCGC PCCCGGCCTG GCGCTGCTGC TCTGCTGCCC GGTGCTCAGC TCCGCGTAGG CGCTG	75
rPTH1	ATGGGGGCCG CCCGGATCGC CCCGGCCTG GCGCTCCTAC TCTGCTGCCC CGCGCTCAGC TCCGCATAIG CGCTG ATGGGGACCG CCCGGATCGC CCCGGCTCGCTCC TCCGCATAIG CGCTG	75 75
mPTH1 hPTH1	ATGGGGACCG CCGGATCGC ACCCGGCCTG CCGCTCGC TCTGCTGCC CGTGCTCAGC TCCGCGTAGG CGCTG	75
dPTH1	GTGGATGGAG ATGAGGTGAT HACGAAAGAG GAHCAGATIGT TCCTGCTGCA CCGHGCGCAG GCHCAHTGCC AFAAG	150
rPTH1	IGTEGANIGUES ADGANIGTUTT INACUAAAGAG GANCAGANIT TCCTGCTGCA CCGNIGCICCAG GCBCANTOTE NDAAG	150
mPTH1	GTGGAGGGG AGGATGTGTT MACGAAAGAG GAACAGATHT TCCTGCTGCA CCGTGCGCAG GCCCAATGTG ADAAG	150
hPTH1	gtegatiedag atteadetdat bactiaaagae gancagatidt tectecteca eegtiecticae eedealiteice inhaala	150
dPTH1	COGCTCAMAG ANGINETICA PAGGACAGOT GACATAATGG ANTCAGACAA AGGATGGOT TCHGCATCOA CATCA	225 225
rPTH1 mPTH1	CTIGOTOANGO ANGITIICTGCA DACAGCAGOO ANCATAATGG AGTCAGACAA EGGCTGGACCA CCNGCATCTIA CETCA CTIGOTOANGO ANGITIICTGCA DACAGCAGOO AACATAATGG AGTCAGACAA NGGCTGGACCT CCNGCATCTIA CETCA	225
hPTH1	CEGCTCAAGG AGGTCCTGCA GAGGCAGGC AGCATAATGG AATCAGACAA GGGATGGACA TCTGCCTTCCA CATCA	225
dPTH1	IGGGAAGCOTA WGAAAGAGAA GGCATIOTIGGG AAGOTCTACC CHIGAGTOCGA DGAGGACAAG GADGTOCCCA CHIGAG	300
rPTH1	IGGGAAGCOO IGGAAAGAAA GGCATIOGGGA AAGTITCTACC CIIGAGTOTAA IGAGAACAAG GAPGTGCCCA CPGGC	388
mPTH1	GEGAAGCDO HEGAAAGADA GECADDOGADA DAGITETACC CHEAGTOTA NGAGAACAAG GAHGTGCCCA CHEGC GEGAAGCDO HEGAAAGATAA GECANDOGADA AACTETACC CHEAGTOTA HEGAGACAAG GAHGCACCCA CHEGC	300 300
hPTH1	Geenverdy devived in actual and work citered of the bandhouse citered	
	Transport of the considered and transported for the consideration of the	375
dPTH1 rPTH1	AGCAGGCADO GAGGGCOCO CONTROL C	375 375
mPTH1	AGCAGGCCCA GAGGGCCCCC CTCTCTCCCC CACTGCCAA ACATCCTTTC CTGGCCATTA GGGCACCAG GTGAA AGCAGCCCCC GAGGGCCCCC CTCTCTCCCA GAGTGGGAAA ACATCCTTTC CTGGCCATTG GGGGCACCAG GTGAA	375
hPTH1	AGCAGGTACC GAGGGCCCCCCTGTCCCGC GANTGGGACC ACATCCTCTGC CTGGCCGCTG GGGCACCAG GTGAG	375
dPTH1	GTGGTGGGTG THEOUTGTCC PGAUTACATT TATGACTTCA ANCACAAAGG CCATGCCTAC PGICGCTGTG ACCGC	450
rPTH1 mPTH1	GTGGTGGGG THOUTTGTCC GGATTACATT TATGACTTCA ATCACAAAGG CCATGCCTAC AGACGCTGG ACCGC GTGGTGGGAG THOUTTGTCC GGATTACATT TATGACTTCA ACCACAAAGG CCATGCCTAC AGACGCTGGG ACCGC	45Ø 45Ø
hPTH1	GTGGTGGTG TECCOTTCC GGACTACATT TATGACTTCA ATTCACAAAGG CCATGCCTAC CGACGCTGTG ACCGC	45Ø
dPTH1	MATGGCAGCT GGGAGGTGGT PCCTIGGACAC AACHGGACGT GGGCCAACTA CAGCGAGTGT GTCAAGTTCC FACC	525
rPTH1	AATGGCAGCT GGGAGGTGGT TICCAGGGCAC AACGGACGT GGGCCAACTA CAGCGAGTGC CTCAAGTTCA THACC	525
mPTH1 hPTH1	AATGGCAGCT GGGAGGTGGT TICCAGGGCCA AACHGGACGT GGGCCAACTA CAGCGAGTGC CTCAAGTTICA TEACC AATGGCAGCT GGGAGGTGGT GCCAGGGCCA AACAGGACGT GGGCCAACTA CAGCGAGTGT GTCAAATTITC TDACC	525 52 5
urini		
ADTU1	MANGAGAGIC GIGAACGGGA GGTGTTTGAC CGCCTINGGCA TGATINTACAC CGTGGGTTAC TCCHTGTCNC THECC	600
dPTH1 rPTH1	AATIGAGAQUE GEGAACGGGA GETATTTGAC CECCTIGGEA TGATCTACAC CETEGGATAC ICCATETCIC TECC	699
mPTH1	IAANIGAGADTO GIGGAACGGGA GGTIATTTGAC CGCCTIGGGCA TGATIOTACAC CGTGGGIATAIT ITCCIATGTOTIC TITIGCC	600
hPTH1	AATIGAGADTO CHIGAACGGGA GETICTTTGAC CECCTICGECA TEATIFITACAC CETEGGICTAC TECCTTETCIC TEGCE	600
dPTH1	TECCTEADOG TEGODORGE CATECTOGOCE TACTTOGOGO GOCTGCACTO CACACGCAAC TACATCCACA TOCACO TECCOTCACO TECC	675 675
rPTH1 mPTH1	freetrandig thighligher cateetilisee talithinage geetgeacte cachegoaac tacatecaca tecat	675
hPTH1	TECETEADES TAGGISTECT CATECTOSEE TAGTITAGGE GECTGEACTE CACECGEAAC TACATECACA TECAC	675
	,	
dPTH1	CTETTCCTET CHTTHATECT INCECECCENE AGCATCTTCE THAAGGACGC PETECTCTAC TCHEGOGICA CECTO	750
rPTH1	ATGITICATED CONTRACT COCCECCEDE AGCATCITICE TRACEGACGE INTECTACE TO THE ACCEPTAGE TO THE AC	75Ø 75Ø
mPTH1 hPTH1	ATETTCCTET CHTHIATECT ECGCECCEDE AGCATCTTCE TEAAGGACGC HETECTCTAC TCHECCTICA CECTE CTETTCCTET CHTHIATECT ECGCECCETE AGCATCTTCE TEAAGGACGC HETECTCTAC TCHECCECCA CECTI	75Ø
ADTU1	GANGAGGONG AGCGCCTCAC HGAGGANGAG HTGCGCGNCA TCGCHCAGCC ACCCCCGCCG CCCACCHCAG FCGCC	825
dPTH1 rPTH1	GANGAGGDD ACCOCCTCAC WGAGGAIGAG INTGCIACATCA TCGCIGCAGG	812
mPTH1	IGATIGAGGDE AGCGCCTCAC DIGAGGAAGAG TITTGCATATICA TCGCDCAGGTGCCDCCTT CCGCC	812
hPTH1	GAMEAGED A ACCECTOR DEAGEN DESCRIPTION OF THE PROPERTY OF THE CONTROL OF THE CONT	824
dPTH1	GGCT ACGOGGGCTG CHOGGTHGGT GTGACCTTCT TCCTTTATTT CCTGGCDACC AACTA	884 887
rPTH1 mPTH1	GECCECTOR TOTAL TOTAL TOTAL PROPERTY OF THE CONTROL OF T	887
hPTH1	TECC GEGT ACGCGGGCTG CHEGGTGGT GTGACCTTCT TCCTTTAGTT CCTGGCCACC AACTA	887
	The second secon	
dPTH1	CTACTGGATT CTGGTGGAGG GCTGTAQT CCATAGTCTC ATCTTCATGG CCTTGTTCTC AGAGAAGAAG TACCT CTACTGGATT CTGGTGGAGG GCTGTAQTT CCADAGCCTC ATCTTCATGG CCTTGTTCTC AGAGAAGAAG TACCT	959
rPTH1	CTACTGGATT CTGGTGGAGG GCTGTACTT CAACACCTC ATCTTCATGG CCTTHTTCTC AGAGAAGAAG TACTT	962 962
* mPTH1 hPTH1	CTACTEGATT CTGGTGGAGG GACTGTACTT ACADAGACTC ATCTTCATGG CCTTHTTCTC AGAGAAGAAG TAICT CTACTGGATT CTGGTGGAGG GACTGTACTT ACADAGACTC ATCTTCATGG CCTTHTTCTC AGAGAAGAAG TAICT	962
OL LUT		

THE THE STATE OF T

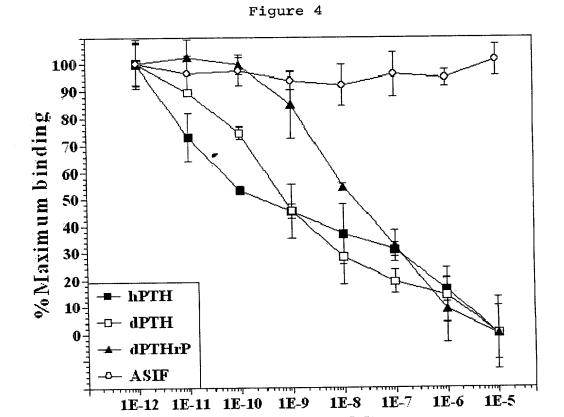
Figure 2 con't

dPTH1 rPTH1 mPTH1 hPTH1	GTGGGGCTTC ACCATCTTIG GCTGGGGTCT ACCAGCIGTC TTCGTGGCTG TGTGGGTGG HGTDAGAGDA ACCHT	1034 1037 1037 1037
dPTH1 rPTH1 mPTH1 hPTH1	GGCCAACAC GGGTGCTGGG ACTTGAGCTC GGGGTACAAG AAGTGGATCA TCCAGGTGCC CATCCTGGGC ICLAT: GGCCAACACT GGGTGCTGGG ACTTGAGCTC GGGGTACAAG AAGTGGATCA TCCAGGTGCC CATCCTGGCA ICLTGT GGCCAACACT GGGTGCTGGG ACCTGAGCTC IGGGGTACAAG AAGTGGATCA TCCAGGTGCC CATCCTGGCA ICLTGT	1109 1112 1112 1112
dPTH1 rPTH1 mPTH1 hPTH1	TETECTCAAC TICATOTITI THIATCANDAT CHICCEGGTO CHICCACHA AGCHICGGA GACCANIGED BECCE TETECTCAAC TICATOTITI THIATCANDAT CHICCEGGTO CHICCACHA AGCHICGGGA GACCANIGED BECCE	1184 1187 1187 1187
dPTH1 rPTH1 mPTH1 hPTH1	GTGTGACAD AGGCAGCAGT ACCGGAAGCT GCTCAGGTCC ACGTTGGTGC TCGTGCCGCT CTTTGGTGTC CACTA	1259 1262 1262 1262
dPTH1 rPTH1 mPTH1 hPTH1	CACOGTOTTO ATGGCOTTEC CETACACCGA GGTCTCAGGG ACATTGTGGC AGATCCAGAT GCATTATGAG ATGCT CACOGTCTTC ATGGCCTTEC CETACACCGA GGTCTCAGGG ACATTGTGGC AGATCCAGAT GCACTATGAG ATGCT	1334 1337 1337 1337
dPTH1 rPTH1 mPTH1 hPTH1	CTTCAACTCC TTCCAGGGAT TTTTTGTTGC CATCATATAC TGTTTCTGCA ATGGTGAGGT CCAGGGAGAG ATTAG CTTCAACTCC TTCCAGGGAT TTTTTGTTGC CATCATATAC TGTTTCTGCA ATGGTGAGGT CCAGGCAGAG ATTAG	1409 1412 1412 1412
dPTH1 rPTH1 mPTH1 hPTH1	GAACTOATEG AGCCGCTEGA CACTEGOGTT GGACTTCAAG CGDAAGGOC GAACTEGGAG TAGCAGCTAC AGCTA GAACTOTTEG AGCCGCTEGA CACTEGOATT GGACTTCAAG CGTAAGGOC GAACTEGGAG TAGCAGCTAC AGCTA	1484 1487 1487 1487
dPTH1 rPTH1 mPTH1 hPTH1	POSOS SENTIFICAÇÃO CAPACITADAS O ASPECAÇÃOS CAPACITADAS ASPECAÇÃOS CAPACAS ESTADOS DE PROPERTO DE PROP	1559 1562 1562 1562
dPTH1 rPTH1 mPTH1 hPTH1	CCTGCT	1634 1616 1616 1619
dPTH1 rPTH1 mPTH1 hPTH1	AGGEDIO ACCCT CDUSTIC EN CACACIAN EN ACTO A CONTRACT OF A CONTRAC	1700 1688 1688 1694
dPTH1 rPTH1 mPTH1 hPTH1	GECTECTEC TELEGACTEG ADGAGGAGGE CTELEGAGADE GAGEGGECTE CELECTECT BEAGGAGGAG TEGGA GECTECTEC TELEGACTEG ATGAGGAGGE CTELEGAGTAT EDGEGGECOC CTICATTETT BEAGGAAGAA TEGGA TEGETECTEC TELEGACTEG ATGAGGAGGE CTETEGAGTAT EDGEGGECOLE CTICATTETT BEAGGAAGAA TEGGA GECTECTEC TELEGACTEG ADGAGGAGGE CTETEGAGTAT GAGEGGECOLE CTICECTEGAT ACAGGAAGAG TEGGA	1775 1763 1763 1769
dPTH1 rPTH1 mPTH1 hPTH1	GACGGTCATG TGA AACAGTCATG TGA AACAGTCATG TGA GACAGTCATG TGA	1788 1776 1776 1782

Seq. ID No. 3A dPTH1; Seq. ID No. 3B rPTH1; Seq. ID No. 3C mPTH1 & Seq. ID No. 3D hPTH1

Figure 3

188	200	299	399	499	595
188	200	300	400	588	591
188	200	300	400	588	593
188	200	300	400	588	593
MGAVRIAP & ALLLCCPVLS SAYALVDADD VMTKEEQIFL LHRAQAQQOK ALKEVUQRPA DIMESDKGVA SASTSGKPRK EKASGKLYPE SHEDKEVPTG MGAARIAPSL ALLLCCPVLS SAYALVDADD VHTKEEQIFL LHRAQAQQOK ULKEVUHTAA NIMESDKGVT PASTSGKPRK EKASGKFYPE SKENKDVPTG MGTARIAPSL ALLLCCPVLS SAYALVDADD VHTKEEQIFL LHRAQAQQOK ULKEVUHTAA NIMESDKGVT PASTSGKPRK EKAPGKFYPE SKENKDVPTG MGTARIAPGL ALLLCCPVLS SAYALVDADD VMTKEEQIFL LHRAQAQQEK RLKEVUQRPA SIMESDKGVT SASTSGKPRK DKASGK LYPE SHEDKEAPTG	SRHRGRPCLP EWDHTLOWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWELVPGH NRTWANYSEC MKRUTNETRE REVFDRLGMI YTVGYSVSLA SRARGRPCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWEVVPGH NRTWANYSEC LKRMTNETRE REVFDRLGMI YTVGYSNSLA SRARGRPCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWEVVPGH NRTWANYSEC LKRMTNETRE REVFDRLGMI YTVGYSVSNSLA SRARGRPCLP EWDHILCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWELVPGH NRTWANYSEC MKRUTNETRE REVFDRLGMI YTVGYSVSLA	SLTVAVLILA YFRRLHCTRN YIHMHUFLSF MLRAVSIFVK DAVLYSGATL DEAERLTEEE LRAIACAPPP PTAAA GYAG CRVAVTFFLY FLATNYYWIL SLTVAVLILA YFRRLHCTRN YIHMHNFLSF MLRAASIFVK DAVLYSGFTL DEAERLTEEE LHIIACVPPP PAAAANGYAG CRVAVTFFLY FLATNYYWIL SLTVAVLILA YFRRLHCTRN YIHMHNFLSF MLRAASIFVK DAVLYSGFTL DEAERLTEEE LHIIACVPPP PAAAANGYAG CRVAVTFFLY FLATNYYWIL SLTVAVLILA YFRRLHCTRN YIHMHUFLSF MLRAVSIFVK DAVLYSGATL DEAERLTEEE LRAIACAPPP PATAAAGYAG CRVAVTFFLY FLATNYYWIL	VEGLYLHSLI FMAFFSEKKY LWGFTVFGWG LPAVFVAVWV SVRATLANTG CWDLSSGNKK WIIQVPILAS IVLNFILFIN INRVLATKLR ETNAGRCDTR VEGLYLHSLI FMAFFSEKKY LWGFTVFGWG LPAVFVAVWV GVRATLANTG CWDLSSGHKK WIIQVPILAS WVLNFILFIN INRVLATKLR ETNAGRCDTR VEGLYLHSLI FMAFFSEKKY LWGFTVFGWG LPAVFVAVWV GVRATLANTG CWDLSSGHKK WIIQVPILAS WVLNFILFIN INRVLATKLR ETNAGRCDTR VEGLYLHSLI FMAFFSEKKY LWGFTVFGWG LPAVFVAVWV SVRATLANTG CWDLSSGNKK WIIQVPILAS IVLNFILFIN INRVLATKLR ETNAGRCDTR	1 QQYRKLUKST LVUMPLFGVH YIVFMALPYT EVSGTLWQYQ MHYEMLFNSF QGFFVAIIYC FCNGEVQAEI KKSWSRWTLA LDFKRKARSG SSSYSYGPNV 1 QQYRKLURST LVUVPLFGVH YTVFMALPYT EVSGTLWQIQ MHYEMLFNSF QGFFVAIIYC FCNGEVQAEI RKSWSRWTLA LDFKRKARSG SSSYSYGPNG 1 QQYRKLUKST LVUMPLFGVH YIVFMALPYT EVSGTLWQYQ MHYEMLFNSF QGFFVAIIYC FCNGEVQAEI KKSWSRWTLA LDFKRKARSG SSSYSYGPNV	SHTSVTNVGP RAGUGLPLSP RULPAAAATT TATTINGHPPI PGHTKPGAFT LPATPPA TAAPKDDGFL NGSCSGLDEE ASAPERPPAL LQEEWETVM SHTSVTNVGP RAGUSLPLSP RULPATT-NGHSQL PGHAKPGAFA TET-ETUPVT MAVPKDDGFL NGSCSGLDEE ASGSARPPPL LQEEWETVM AHTSVTNVGP RAGUSLPLSP RULPATT-NGHSQL PGHAKPGAFA IEN-ETIPVT MTVPKDDGFL NGSCSGLDEE ASGSARPPPL LQEEWETVM SHTSVTNVGP RAGUGLPLSP RULPTATTINGHPQL PGHAKPGTFA LETLETTPPA MAAPKDDGFL NGSCSGLDEE ASGPERPPAL LQEEWETVM Seg. ID No. 2A dPTH1; Seq. ID No. 2B rPTH1; Seq. ID No. 2D abth1.
dPTH1	dPTH1	dPTH1	dPTH1	dPTH1	dРТН1
rPTH1	rPTH1	rPTH1	rPTH1	rPTH1	rРТН1
mPTH1	mPTH1	mPTH1	mPTH1	mPTH1	mРТН1
hPTH1	hPTH1	hPTH1	hPTH1	hPTH1	hРТН1



[Peptide] (M)

